

PCT09

RAW SEQUENCE LISTING

DATE: 10/23/2001

PATENT APPLICATION: US/09/807,660A

TIME: 10:13:35

Input Set : A:\09-807660 Sequence Listing.txt

Output Set: N:\CRF3\10232001\I807660A.raw

3 <110> APPLICANT: Maliszewski, Charles R.
 4 Gayle III, Richard B.
 5 Marcus, Aaron J.
 6 Immunex Corporation
 7 Cornell Research Foundation, Inc.
 9 <120> TITLE OF INVENTION: Methods of Inhibiting Platelet Activation and
 10 Recruitment
 12 <130> FILE REFERENCE: 23,495 PCT
 14 <140> CURRENT APPLICATION NUMBER: US 09/807,660A
 15 <141> CURRENT FILING DATE: 2001-04-16
 17 <150> PRIOR APPLICATION NUMBER: US 60/104,585
 18 <151> PRIOR FILING DATE: 1998-10-16
 20 <150> PRIOR APPLICATION NUMBER: US 60/107,466
 21 <151> PRIOR FILING DATE: 1998-11-06
 23 <150> PRIOR APPLICATION NUMBER: US 60/149,010
 24 <151> PRIOR FILING DATE: 1999-08-13
 26 <160> NUMBER OF SEQ ID NOS: 31
 28 <170> SOFTWARE: PatentIn Ver.. 2.0
 30 <210> SEQ ID NO: 1
 31 <211> LENGTH: 1599
 32 <212> TYPE: DNA
 33 <213> ORGANISM: Homo sapiens
 35 <220> FEATURE:
 36 <221> NAME/KEY: CDS
 37 <222> LOCATION: (67)..(1596)
 39 <400> SEQUENCE: 1
 40 ccacaccaag cagcggtctgg ggggggggaaa gacgaggaaa gaggaggaaa acaaaagctg 60
 42 ctacttt atg gaa gat aca aag gag tct aac gtg aag aca ttt tgc tcc 108
 43 Met Glu Asp Thr Lys Glu Ser Asn Val Lys Thr Phe Cys Ser
 44 1 5 10
 46 aag aat atc cta gcc atc ctt ggc ttc tcc tct atc ata gct gtg ata 156
 47 Lys Asn Ile Leu Ala Ile Leu Gly Phe Ser Ser Ile Ile Ala Val Ile
 48 15 20 25 30
 50 gct ttg ctt gct gtg ggg ttg acc cag aac aaa gca ttg cca gaa aac 204
 51 Ala Leu Leu Ala Val Gly Leu Thr Gln Asn Lys Ala Leu Pro Glu Asn
 52 35 40 45
 54 gtt aag tat ggg att gtg ctg gat gcg ggt tct tct cac aca agt tta 252
 55 Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu
 56 50 55 60
 58 tac atc tat aag tgg cca gca gaa aag gag aat gac aca ggc gtg gtg 300
 59 Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val
 60 65 70 75
 62 cat caa gta gaa gaa tgc agg gtt aaa ggt cct gga atc tca aaa ttt 348
 63 His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe
 64 80 85 90
 66 gtt cag aaa gta aat gaa ata ggc att tac ctg act gat tgc atg gaa 396
 67 Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu

ENTERED

P.5

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68	95		100		105		110	
70	aga gct agg gaa gtg att cca agg tcc cag cac caa gag aca ccc gtt	444						
71	Arg Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val							
72		115	120	125				
74	tac ctg gga gcc acg gca ggc atg cgg ttg ctc agg atg gaa agt gaa	492						
75	Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu							
76		130	135	140				
78	gag ttg gca gac agg gtt ctg gat gtg gtg gag agg agc ctc agc aac	540						
79	Glu Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn							
80		145	150	155				
82	tac ccc ttt gac ttc cag ggt gcc agg atc att act ggc caa gag gaa	588						
83	Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu							
84		160	165	170				
86	ggt gcc tat ggc tgg att act atc aac tat ctg ctg ggc aaa ttc agt	636						
87	Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser							
88	175	180	185	190				
90	cag aaa aca agg tgg ttc agc ata gtc cca tat gaa acc aat aat cag	684						
91	Gln Lys Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln							
92		195	200	205				
94	gaa acc ttt gga gct ttg gac ctt ggg gga gcc tct aca caa gtc act	732						
95	Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr							
96		210	215	220				
98	ttt gta ccc caa aac cag act atc gag tcc cca gat aat gct ctg caa	780						
99	Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln							
100		225	230	235				
102	ttt cgc ctc tat ggc aag gac tac aat gtc tac aca cat agc ttc ttg	828						
103	Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu							
104		240	245	250				
106	tgc tat ggg aag gat cag gca ctc tgg cag aaa ctg gcc aag gac att	876						
107	Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile							
108	255	260	265	270				
110	cag gtt gca agt aat gaa att ctc agg gac cca tgc ttt cat cct gga	924						
111	Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly							
112		275	280	285				
114	tat aag aag gta gtg aac gta agt gac ctt tac aag acc ccc tgc acc	972						
115	Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr							
116		290	295	300				
118	aag aga ttt gag atg act ctt cca ttc cag cag ttt gaa atc cag ggt	1020						
119	Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly							
120		305	310	315				
122	att gga aac tat caa caa tgc cat caa agc atc ctg gag ctc ttc aac	1068						
123	Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn							
124		320	325	330				
126	acc agt tac tgc cct tac tcc cag tgt gcc ttc aat ggg att ttc ttg	1116						
127	Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu							
128	335	340	345	350				
130	cca cca ctc cag ggg gat ttt ggg gca ttt tca gct ttt tac ttt gtg	1164						
131	Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val							
132		355	360	365				

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134 atg aag ttt tta aac ttg aca tca gag aaa gtc tct cag gaa aag gtg 1212
135 Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val
136          370          375          380
138 act gag atg atg aaa aag ttc tgt gct cag cct tgg gag gag ata aaa 1260
139 Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys
140          385          390          395
142 aca tct tac gct gga gta aag gag aag tac ctg agt gaa tac tgc ttt 1308
143 Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe
144          400          405          410
146 tct ggt acc tac att ctc tcc ctc ctt ctg caa ggc tat cat ttc aca 1356
147 Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr
148 415          420          425          430
150 gct gat tcc tgg gag cac atc cat ttc att ggc aag atc cag ggc agc 1404
151 Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser
152          435          440          445
154 gac gcc ggc tgg act ttg ggc tac atg ctg aac ctg acc aac atg atc 1452
155 Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile
156          450          455          460
158 cca gct gag caa cca ttg tcc aca cct ctc tcc cac tcc acc tat gtc 1500
159 Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr Tyr Val
160          465          470          475
162 ttc ctc atg gtt cta ttc tcc ctg gtc ctt ttc aca gtg gcc atc ata 1548
163 Phe Leu Met Val Leu Phe Ser Leu Val Leu Phe Thr Val Ala Ile Ile
164          480          485          490
166 ggc ttg ctt atc ttt cac aag cct tca tat ttc tgg aaa gat atg gta 1596
167 Gly Leu Leu Ile Phe His Lys Pro Ser Tyr Phe Trp Lys Asp Met Val
168 495          500          505          510
170 tag 1599
173 <210> SEQ ID NO: 2
174 <211> LENGTH: 510
175 <212> TYPE: PRT
176 <213> ORGANISM: Homo sapiens
178 <400> SEQUENCE: 2
179 Met Glu Asp Thr Lys Glu Ser Asn Val Lys Thr Phe Cys Ser Lys Asn
180 1 5 10 15
182 Ile Leu Ala Ile Leu Gly Phe Ser Ser Ile Ile Ala Val Ile Ala Leu
183 20 25 30
185 Leu Ala Val Gly Leu Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys
186 35 40 45
188 Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile
189 50 55 60
191 Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln
192 65 70 75 80
194 Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln
195 85 90 95
197 Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala
198 100 105 110
200 Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu
201 115 120 125

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203 Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu
204      130      135      140
206 Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro
207 145      150      155      160
209 Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala
210      165      170      175
212 Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys
213      180      185      190
215 Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr
216      195      200      205
218 Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val
219      210      215      220
221 Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg
222 225      230      235      240
224 Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr
225      245      250      255
227 Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val
228      260      265      270
230 Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys
231      275      280      285
233 Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg
234      290      295      300
236 Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly
237 305      310      315      320
239 Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser
240      325      330      335
242 Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro
243      340      345      350
245 Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys
246      355      360      365
248 Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu
249      370      375      380
251 Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser
252 385      390      395      400
254 Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly
255      405      410      415
257 Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp
258      420      425      430
260 Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala
261      435      440      445
263 Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala
264      450      455      460
266 Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr Tyr Val Phe Leu
267 465      470      475      480
269 Met Val Leu Phe Ser Leu Val Leu Phe Thr Val Ala Ile Ile Gly Leu
270      485      490      495
272 Leu Ile Phe His Lys Pro Ser Tyr Phe Trp Lys Asp Met Val
273      500      505      510
276 <210> SEQ ID NO: 3

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277 <211> LENGTH: 476
278 <212> TYPE: PRT
279 <213> ORGANISM: Artificial Sequence
281 <220> FEATURE:
282 <223> OTHER INFORMATION: Description of Artificial Sequence: Fusion
283     construct of human CD39
285 <400> SEQUENCE: 3
286 Met Ala Thr Ser Trp Gly Thr Val Phe Phe Met Leu Val Val Ser Cys
287   1           5           10           15
289 Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe Glu Gly
290           20           25           30
292 Ile Phe Leu Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys
293           35           40           45
295 Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile
296           50           55           60
298 Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln
299           65           70           75           80
301 Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln
302           85           90           95
304 Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala
305           100          105          110
307 Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu
308           115          120          125
310 Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu
311           130          135          140
313 Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro
314           145          150          155          160
316 Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala
317           165          170          175
319 Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys
320           180          185          190
322 Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr
323           195          200          205
325 Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val
326           210          215          220
328 Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg
329           225          230          235          240
331 Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr
332           245          250          255
334 Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val
335           260          265          270
337 Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys
338           275          280          285
340 Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg
341           290          295          300
343 Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly
344           305          310          315          320
346 Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser
347           325          330          335

```

Use of n and / or Xaa has been detected in the
Sequence Listing. Review the Sequence Listing
to ensure a corresponding explanation is present
in the <220> to <223> fields of each sequence
using n or Xaa.

VERIFICATION SUMMARY

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L:398 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4